

SEQUENCE LISTING

<110> Majumder, Arunendra  
Manoj, Majee

<120> A salt tolerant L-myo-inositol 1-phosphate synthase  
and the process of obtaining the same

<130> 4544-051674

<140> US 10/538,423

<141> 2005-06-10

<150> PCT/IN2003/000065

<151> 2003-03-21

<160> 3

<170> MicrosoftWord 2003

<210> 1

<211> 1536

<212> DNA

<213> Porteresia coarctata

<220>

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cggcgcctcg 120

cgctgggtcg tccgccccaa gtccgtccag taccacttca ggaccagcac  
cacgtcccc 180

aagctcgggg tcatgctcgt ggggtggggc ggcaacaacg gctcaacgct  
gacggctggg 240

gtcatcgcca gcaggagggg aatctcatgg gcgaccaagg acaagggtgca  
gcaagccaac 300

tactatggct cactcaccca ggcgtccacc atcagggtag gaagctacaa  
cggggaggag 360

atctacgcgc ctttcaagag cctcctgccc atggtgaacc ctgatgacct  
tgtgttcggg 420

ggctgggaca ttagcaacat gaacctggct gatgctatga ccagggccaa  
ggtgctggac 480

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cctggcatct 540

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ccaagaagga gcagatgggg cagatcatca aaggacatca gggagttcaa  
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ccgttcaata 840

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taaaaaaaaa 900

ctgcctgata cgggggggatt aattcaaaaa aggggcaaac caaaaaaaaa  
aaccggcttg 960

gttgatttcc tcatgggtgc tggaaataaag cccacctcaa ttgtcagtta  
caaccacttg 1020

gggaataatg atggcacgaa cttttctgcg ccgcaaacat tccgatccaa  
ggagatctcc 1080

aaaagcagcg tggtcgatga catggtctca agcaatgcta tcctctacga  
gcctggcgag 1140

catcctgata atgttgctgt gattaagtat gtgccgtacg tcggagacag  
caagagggcc 1200

atggatgagt acacctcaga gatcttcatg gggggtaaga acaccatcgt  
gctgcacaac 1260

acctgcgagg actcgctcct tgctgcacca atcattcttg acctgggtgct  
cctggccgag 1320

ctcagcacta ggattcagct gaaaggcgag ggagaggaga aattccattc  
cttccatcca 1380

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cacaccagtg 1440

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<211> 510

<212> PRT

<213> Oryza sativa

<220>

<400> 2

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Gly  
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Ala Ala Glu Ile Glu Ser Asp Tyr Gln Tyr Asp Thr Thr Glu Leu  
Val  
20 25 30

His Glu Ser His Asp Gly Ala Ser Arg Tyr Ile Val Arg Pro Lys  
Ser  
35 40 45

Val Arg Tyr Asn Phe Arg Thr Thr Thr Thr Val Pro Lys Leu Gly  
Val  
50 55 60

Met Leu Val Gly Tyr Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala  
Gly  
65 70 75  
80

Val Ile Ala Asp Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys  
Val  
85 90 95

Gln Gln Ala Asn Tyr Tyr Gly Ser Leu Thr Gln Ala Ser Thr Ile  
Arg

100

105

110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser  
Leu

115

120

125

Leu Pro Met Val Asn Pro Asp Asp Leu Val Phe Gly Gly Trp Asp  
Ile

130

135

140

Ser Asn Met Asn Leu Ala Asp Ala Met Thr Arg Ala Lys Val Leu  
Asp

145

150

155

160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Val  
Pro

165

170

175

Leu Pro Gly Ile Tyr Asp Pro Asp Val Ile Ala Ala Asn Gln Gly  
Ser

180

185

190

Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Lys Glu Gln Met Glu  
Gln

195

200

205

Ile Ile Lys Asp Ile Arg Glu Phe Lys Glu Lys Ser Lys Val Asp  
Lys

210

215

220

Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Val  
Cys

225

230

235

240

Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ser Val Asp  
Lys

245

250

255

Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys  
Val

260

265

270

Met Glu Gly Ile Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe  
Val

275	280	285
Pro Gly Leu Ile Asp Leu Ala Ile Lys Asn Asn Cys Leu Ile Gly		
Gly		
290	295	300
Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val		
Asp		
305	310	315
320		
Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr		
Asn		
325	330	335
His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr		
Phe		
340	345	350
Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val		
Ser		
355	360	365
Ser Asn Ala Ile Leu Tyr Glu Leu Gly Glu His Pro Asp His Val		
Val		
370	375	380
Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met		
Asp		
385	390	395
400		
Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val		
Leu		
405	410	415
His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu		
Asp		
420	425	430
Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu Lys Ala		
Glu		
435	440	445
Gly Glu Glu Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu		
Ser		
450	455	460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val  
 Asn  
 465 470 475  
 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala  
 Cys  
 485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys  
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<210> 3  
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 <213> *Porteresia coarctata*

<220>

<400> 3

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 Gly  
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Ala Ala Glu Ile Glu Ser Glu Tyr Arg Tyr Asp Thr Thr Glu Leu  
 Val  
 20 25 30

His Glu Ser His Asp Gly Ala Ser Arg Trp Val Val Arg Pro Lys  
 Ser  
 35 40 45

Val Gln Tyr His Phe Arg Thr Ser Thr Thr Val Pro Lys Leu Gly  
 Val  
 50 55 60

Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala  
 Gly  
 65 70 75  
 80

Val Ile Ala Ser Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys  
 Val  
 85 90 95

Gln Gln Ala Asn Tyr Tyr Gly Ser Leu Thr Gln Ala Ser Thr Ile  
Arg

100

105

110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser  
Leu

115

120

125

Leu Pro Met Val Asn Pro Asp Asp Leu Val Phe Gly Gly Trp Asp  
Ile

130

135

140

Ser Asn Met Asn Leu Ala Asp Ala Met Thr Arg Ala Lys Val Leu  
Asp

145

150

155

160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Trp Cys  
Leu

165

170

175

Ser Leu Ala Ser Met Ile Pro Thr Ser Ser Pro Leu Thr Arg Asp  
Pro

180

185

190

Ala Arg Thr Met Ser Ser Arg Glu Pro Arg Arg Ser Arg Trp Gly  
Arg

195

200

205

Ser Ser Lys Asp Ile Arg Glu Phe Lys Glu Asn Asn Lys Met Asp  
Lys

210

215

220

Ala Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Asn Asn Cys  
Leu

225

230

235

240

Cys Leu Gly Leu Met Thr Asn Gly Lys Pro Ser Ala Ser Val Asp  
Arg

245

250

255

Asn Gln Ala Glu Ile Ser Pro Ser Thr Leu Tyr Cys His Cys Leu  
Ala

260

265

270

Ser Leu Glu Gly Val Arg Ser Ile Thr Gly Ala Leu Lys Lys Lys  
Ser

275

280

285

Trp Pro Gly Ile Asp Asp Leu Ala Ile Lys Lys Lys Leu Pro Asp  
Pro

290

295

300

Gly Gly Leu Ile Gln Lys Arg Gly Lys Pro Lys Lys Lys Thr Gly  
Leu

305

310

315

320

Val Asp Phe Leu Met Gly Ala Gly Ile Lys Pro Thr Ser Ile Val  
Ser

325

330

335

Tyr Asn His Leu Gly Asn Asn Asp Gly Thr Asn Leu Ser Ala Pro  
Gln

340

345

350

Thr Phe Arg Ser Lys Glu Ile Ser Lys Ser Ser Val Val Asp Asp  
Met

355

360

365

Val Ser Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp  
His

370

375

380

Val Val Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg  
Ala

385

390

395

400

Met Asp Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Asn Thr  
Ile

405

410

415

Val Leu His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile  
Ile

420

425

430

Leu Asp Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Gln Leu  
Lys

435

440

445



Gly Glu Gly Glu Glu Lys Phe His Ser Phe His Pro Val Ala Thr  
Ile

450

455

460

Leu Ser Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro  
Val

465

470

475

480

Val Asn Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met  
Arg

485

490

495

Ala Cys Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr  
Lys

500

505

510